

09-29-00

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UTILITY PATENT APPLICATION TRANSMITTAL
(Large Entity)*(Only for new nonprovisional applications under 37 CFR 1.53(b))*Docket No.
BMID9975USTotal Pages in this Submission
64**TO THE ASSISTANT COMMISSIONER FOR PATENTS**Box Patent Application
Washington, D.C. 20231

Transmitted herewith for filing under 35 U.S.C. 111(a) and 37 C.F.R. 1.53(b) is a new utility patent application for an invention entitled:

PROCESS FOR THE RECOMBINANT PRODUCTION OF HOLO-CITRATE LYASE

and invented by:

Michael BOTT, Peter DIMROTH and Karin SCHNEIDER**If a CONTINUATION APPLICATION, check appropriate box and supply the requisite information:**☒ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No.: _____

Which is a:

☒ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No.: _____

Which is a:

☒ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No.: _____

Enclosed are:

Application Elements

1. ☐ Filing fee as calculated and transmitted as described below
2. ☒ Specification having 27 pages and including the following:
 - a. ☒ Descriptive Title of the Invention
 - b. ☐ Cross References to Related Applications *(if applicable)*
 - c. ☐ Statement Regarding Federally-sponsored Research/Development *(if applicable)*
 - d. ☐ Reference to Microfiche Appendix *(if applicable)*
 - e. ☒ Background of the Invention
 - f. ☒ Brief Summary of the Invention
 - g. ☒ Brief Description of the Drawings *(if drawings filed)*
 - h. ☒ Detailed Description
 - i. ☒ Claim(s) as Classified Below
 - j. ☒ Abstract of the Disclosure

UTILITY PATENT APPLICATION TRANSMITTAL
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64

Application Elements (Continued)

3. ☒ Drawing(s) *(when necessary as prescribed by 35 USC 113)*

a. ☐ Formal Number of Sheets _____

b. ☒ Informal Number of Sheets 2

4. ☒ Oath or Declaration

a. ☐ Newly executed *(original or copy)* ☒ Unexecuted

b. ☐ Copy from a prior application (37 CFR 1.63(d)) *(for continuation/divisional application only)*

c. ☒ With Power of Attorney ☐ Without Power of Attorney

d. ☐ DELETION OF INVENTOR(S)

Signed statement attached deleting inventor(s) named in the prior application,
see 37 C.F.R. 1.63(d)(2) and 1.33(b).

5. ☐ Incorporation By Reference *(usable if Box 4b is checked)*

The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. ☐ Computer Program in Microfiche *(Appendix)*

7. ☐ Nucleotide and/or Amino Acid Sequence Submission *(if applicable, all must be included)*

a. ☐ Paper Copy

b. ☐ Computer Readable Copy *(identical to computer copy)*

c. ☐ Statement Verifying Identical Paper and Computer Readable Copy

Accompanying Application Parts

8. ☐ Assignment Papers *(cover sheet & document(s))*

9. ☐ 37 CFR 3.73(B) Statement *(when there is an assignee)*

10. ☐ English Translation Document *(if applicable)*

11. ☐ Information Disclosure Statement/PTO-1449 ☐ Copies of IDS Citations

12. ☒ Preliminary Amendment *(to follow)*

13. ☒ Acknowledgment postcard

14. ☒ Certificate of Mailing

☐ First Class ☒ Express Mail *(Specify Label No.):* EL315020614US

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Accompanying Application Parts (Continued)

15. ☒ Certified Copy of Priority Document(s) (if foreign priority is claimed)
16. ☒ Additional Enclosures (please identify below):

General Appointment of Representative for U.S. Patent and Trademark Office Matters.

Fee Calculation and Transmittal

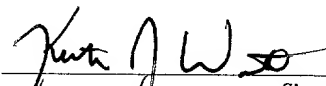
CLAIMS AS FILED

For	#Filed	#Allowed	#Extra	Rate	Fee
Total Claims		- 20 =	0	x \$18.00	\$0.00
Indep. Claims		- 3 =	0	x \$78.00	\$0.00
Multiple Dependent Claims (check if applicable) <input type="checkbox"/>					\$0.00
BASIC FEE					\$0.00
OTHER FEE (specify purpose)					\$0.00
TOTAL FILING FEE					\$0.00

- ☐ A check in the amount of _____ to cover the filing fee is enclosed.
- ☐ The Commissioner is hereby authorized to charge and credit Deposit Account No. _____ as described below. A duplicate copy of this sheet is enclosed.
- ☐ Charge the amount of _____ as filing fee.
 - ☐ Credit any overpayment.
 - ☐ Charge any additional filing fees required under 37 C.F.R. 1.16 and 1.17.
 - ☐ Charge the issue fee set in 37 C.F.R. 1.18 at the mailing of the Notice of Allowance, pursuant to 37 C.F.R. 1.311(b).

Dated: September 28, 2000

cc:



Signature

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CERTIFICATE OF MAILING BY "EXPRESS MAIL" (37 CFR 1.10)Applicant(s): **Michael BOTT, et al.**

Docket No.

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U.S. PTO

09/672265**09/28/00**

Serial No.

To Be Assigned

Filing Date

September 28, 2000

Examiner

To Be Assigned

Group Art Unit

To Be Assigned

Invention: **PROCESS FOR THE RECOMBINANT PRODUCTION OF HOLO-CITRATE LYASE**

I hereby certify that this

Utility Patent Application*(Identify type of correspondence)*

is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 in an envelope addressed to: The Assistant Commissioner for Patents, Washington, D.C. 20231 on **September 28, 2000.**

*(Date)***Rose Edwards***(Typed or Printed Name of Person Mailing Correspondence)**(Signature of Person Mailing Correspondence)***EL315020614US***("Express Mail" Mailing Label Number)***Note: Each paper must have its own certificate of mailing.**

Process for the recombinant production of holo-citrate lyase

The enzyme citrate lyase (EC4.1.3.6) is regarded as a key enzyme of anaerobic citrate degradation and can accordingly be isolated from a number of different prokaryotic cells. The enzyme catalyses the cleavage of citrate into acetate and oxaloacetate. Furthermore it is known that the enzyme complex of the citrate lyase enzyme that has been best examined to date from *Klebsiella pneumoniae* (formally: *Klebsiella aerogenes*) is composed of six copies of each of three different subunits and namely an α , β and γ subunit, of a molecular weight of about 550,000 Dalton. In addition it is known that the catalytically active centre is located in the α and β subunit, whereas the γ subunit has the binding site for the prosthetic group 2'-(5"phosphoribosyl)-3'-dephospho CoA. This prosthetic group is bound to the serine residue 14 via a phosphodiester bond.

The citrate lyase enzyme is required in high purity for most applications which are primarily for clinical chemistry and food analysis. Hence the aim is to over-produce the enzyme in an active form in certain host cells by recombinant methods and to isolate it from these cells. Such a process has not yet been described or made known in other ways. Hence citrate lyase is nowadays usually isolated from *Klebsiella pneumoniae* cells which had been cultured under anaerobic conditions using citrate as the only carbon and energy source. The citrate lyase genes from *Klebsiella pneumoniae* have been

cloned and sequenced (M. Bott and P. Dimroth, Mol. Microbiol. Vol. 14, 347-356 (1994)). These genes are part of the citC operon which is composed of the five genes citCDEFG. The citC gene codes for citrate lyase ligase which catalyses the formation of an acetyl thioester. The genes citD, citE and citF code for the gamma, beta and alpha subunit of citrate lyase. The protein coded by citG is involved in the biosynthesis of the prosthetic group. Furthermore it is known that the citC operon is induced in the absence of oxygen and in the presence of citrate and Na⁺ ions; moreover the expression is strongly dependent on the citA/citB regulation system (M. Bott et al., Mol. Microbiol. Vol. 18, 533-546 (1995); M. Meyer et al., J. Mol. Biol. Vol. 269, 719-731 (1997)).

Expression of the genes coding for citrate lyase from *Klebsiella pneumoniae* which would preferably be carried out in prokaryotic cells such as *E. coli* for practical reasons, results in an inactive but nevertheless soluble form of the enzyme (M. Bott and P. Dimroth, Mol. Microbiol. Vol. 14, 347-356 (1994)). The recombinant apo-citrate lyase enzyme can be activated to form the holo-enzyme by subsequent addition of acetyl coenzyme A which is known as a substituent for the acetyl thioester of the native prosthetic group 2'-(5"-phosphoribosyl)-3'-dephospho CoA. However, such an additional activation measure is complicated and laborious. Moreover the necessity to add acetyl CoA is unsuitable for the commercial distribution of citrate lyase or the apo form since the substance decomposes when stored for long periods at 4°C.

Hence the object of the invention is to provide a recombinant, soluble and at the same time active holo-

citrate lyase which eliminates the disadvantages of the known methods.

The object is achieved by a process for the production of a protein with citrate lyase activity by expressing a suitable plasmid in a host organisms whereby the plasmid contains the information of a gene cluster composed of at least six genes and an inducible promoter. The genes comprising the gene cluster code for certain subunits of the protein with citrate lyase activity and/or for a component which participates in the biosynthesis of the complete enzyme. In particular a suitable plasmid contains the genes citC, citD, citE, citF, citG and a DNA fragment that can for example be obtained from E. coli which is located between the genes citF and citG on the E. coli citrate lyase gene cluster. The genes citD, citE and citF code for the corresponding γ , β and α subunits of the enzyme and have molecular weights of about 11,000 Dalton, 32,000 Dalton and 55,000 Dalton. According to the invention it is preferred that one of the genes represents a DNA fragment which codes for a protein containing the motif G(A)-R-L-X-D-L(I)-D-V. A corresponding DNA fragment is particularly preferred which codes for a protein with a molecular weight of about 20,000 Dalton.

In addition it has proven to be advantageous when one gene and optionally a further gene fused to the first gene of the genes comprising the gene cluster is derived from a different organism than the other genes. In particular it has proven to be advantageous when the DNA fragment citX or genes homologous to citX located between citF and citG on the E. coli citrate lyase gene cluster are derived from E. coli, Klebsiella pneumoniae, Haemophilus influenzae or Leuconostoc mesenteroides and

when one or several of the other genes are derived from the microorganism that is specific for the isolated protein having citrate lyase activity which is for example *Klebsiella pneumoniae*. In *Haemophilus influenza*, *Leuconostoc mesenteroides* (S. Bekal et al., J. Bacteriol. Vol. 180, 647-654 (1998)) and *Leuconostoc paramesenteroides* (M. Martin et al., FEMS Microbiol. Lett. Vol. 174, 231-238 (1999)) the genes *citX* and *citG* occur in a fused form. Thus corresponding fusion genes contain the information of two genes. The resulting proteins have a molecular weight of about 52,000 Dalton, have the activities of *E. coli* CitX and CitG and are thus bifunctional. In the absence of the *citX* gene or of a gene homologous to *citG* or of a corresponding *citX* fusion gene, only the low-molecular apo form (MW 12,000 Dalton, SDS-PAGE) but not the holo form of citrate lyase (MW 14,500 Dalton, SDS-PAGE) could be detected after expression.

According to the invention prokaryotes as well as eukaryotes have proven to be suitable as the host organism. The fact that a soluble active citrate lyase can now be produced in prokaryotes such as e.g. *E. coli* in a simple manner and in adequate yields without additional activation measures is a major advantage.

Hence it was possible to show that by cloning the entire *E. coli* *citCDEFXG* gene cluster under the control of an inducible promoter such as e.g. the *lac*, *lac UV5*, *T5*, *tac* or *T7* promoter, an active enzyme can be expressed having citrate lyase activity even under non-oxygen limiting conditions. Cell extracts containing appropriate expression plasmids result in citrate lyase activities of about 4 to 5 U/mg protein in the cell-free extract whereas cells without recombinant citrate lyase

have no citrate lyase activity when grown aerobically.

In addition the invention concerns the simultaneous expression of the citCDEFG gene cluster from *Klebsiella pneumoniae* and of the citX gene obtainable from *E. coli* by which means it is possible to obtain a corresponding citrate lyase in an active form even in prokaryotes and in particular in *E. coli*.

By this means it was possible to achieve an activity of about 8 U/mg total protein in a cell-free extract under aerobic growth conditions.

The holo-enzyme is purified by methods known to a person skilled in the art. About 100 to 120 μ g soluble protein with citrate lyase activity can be obtained from about 1 g of cells (wet weight) using the process according to the invention. The protein determination was carried out according to P.K. Smith et al., Anal. Biochem. Vol. 150, 76-85 (1985) using ovalbumin as a standard. The specific activity of the citrate lyase is ca. 70 U/ml protein (M. Single and P.A. Srere, J. Biol. Chem. Vol. 251 (10), 2911-2615 (1976)). The activity of the holo-enzyme that can be obtained by the process according to the invention is thus ca. 0.5 to 3-fold higher than the activity that was achieved with acetyl CoA and apo-citrate lyase.

Hence the process according to the invention provides for the first time a recombinant protein with improved citrate lyase activity that is both soluble and active.

Furthermore the invention concerns a test kit for the determination of citric acid which is composed

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essentially of the following components: a protein obtainable by the process according to the invention with citrate lyase activity, at least one protein with hydrogen-transferring activity, nicotinamide-adenine dinucleotide or an appropriate derivative in a reduced form and optionally suitable stabilizers, activators and/or substances to avoid or reduce interferences i.e. components or reactions which mask or interfere with the actual reaction as well as suitable buffer solutions. In particular L-malate dehydrogenase and L-lactate dehydrogenase come into consideration as proteins with hydrogen-transferring activity. Those substances, additives or measures which help to avoid or at least to delay the degradation of a property or activity that is important for the determination are in principle suitable as stabilizers. Especially when only small amounts of sample material are available or if the samples are very dilute it can be advantageous to add activators.

An additional subject matter of the invention is the use of the recombinant soluble protein with citrate lyase activity to determine citric acid in clinical chemistry, food analysis and as a purity test for cosmetics. In clinical chemistry a corresponding enzymatic test is used primarily to examine fertility and for therapeutic monitoring of patients with kidney stones. In food analysis the most important application is analysis of wines and fruit juices.

The enzymatic method is based on the cleavage of citrate by the enzyme citrate lyase in the presence of Mg^{2+} ions to form oxaloacetate and acetate. In the presence of hydrogen-transferring enzymes such as L-malate dehydrogenase and L-lactate dehydrogenase, oxaloacetate

and its decarboxylation product pyruvate are reduced by reduced NADH or NADPH to form L-malate and L-lactate. The amount of NADH or NADPH is proportional to the amount of citrate and is measured at 334 nm, 340 nm or 365 nm.

Hence the invention also concerns a corresponding test kit for the determination of citric acid which, apart from suitable buffer solutions, contains a recombinant protein with citrate lyase activity, one or several hydrogen-transferring enzymes and a nicotinamide adenine dinucleotide or a corresponding derivative in a reduced form and optionally suitable stabilizers such as thiol reagents.

Figure legends

Figure 1:

A: Function of the various subunits in a reaction catalysed by citrate lyase and activation of the enzyme by citrate lyase ligase. HS-R denotes a prosthetic group.

B. Structure of the prosthetic group of citrate lyase 2'-(5"-phosphoribosyl)-3'-phospho-CoA.

Figure 2:

Citrate lyase gene cluster from *Klebsiella pneumoniae* (K.p.), *Escherichia coli* (E.c.) *Haemophilus influenzae* (H.i.) and *Leuconostoc mesenteroides* (L.m.). Gene sequences that are homologous to E. coli citX are shown by the light grey shading.

INFORMATION FOR SEQ ID NO. 1:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 36 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

5'- CCCTCTAGAGAACAACATTCGTTGCAAATCGATAAC - 3'

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 38 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

5'- CCGCGAATTCTTAGTTCCACATGGCGAGAATCGGCCAG -3'

INFORMATION FOR SEQ ID NO. 3:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 5484 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

1 GAACAACATT CGTTGCAAAT CGATAACAAC ATGCACCTTC AGGATACTAT
 start site
51 TTATTATGTT CGGCAATGAT ATTTTCACCC GCGTAAAACG TTCAGAAAAT
101 AAAAAAATGG CGGAAATCGC CCAATTCCTG CATGAAAATG ATTTGAGCGT
151 TGACACCACA GTCGAAGTAT TTATTACCGT AACCCGCGAT GAAAAGCTTA
201 TCGCGTGCGG TGAATTGCC GGAAATATTA TTAAATGCGT TGCTATCAGT
251 GAATCCGTCC GCGGTGAAGG ACTGGCGCTG ACATTAGCCA CTGAATTGAT
301 AAACCTCGCC TATGAGCGGC ACAGCACGCA TCTGTTTATT TATACCAAAA
351 CCGAATACGA GCGCTGTTC CGCCAGTGCG GTTTTTCAC GCTGACCAGC
401 GTACCCGCGG TGATGGTGCT GATGGAAAAC AGCGCCACGC GACTGAAACG
451 CTATGCCGAA TCGCTGAAAA AATTTCGTCA TCCAGGGAAC AAGATTGGCT
501 GCATTGTGAT GAACGCCAAT CCCTTTACGA ATGGTCACCG TTATCTGATT
551 CAACAGGCTG CGGCACAGTG CCACTGGTTG CATCTGTTTT TAGTCAAAGA
601 AGATTCTTCA CGCTTCCCCT ATGAAGACCG GCTGGATTTC GTGTTAAAAG
651 GCACCGCCGA TATTCCACGC CTGACTGTGC ATCGTGGCTC CGAATACATC
701 ATCTCCCGCG CTACGTTCCC TTGCTACTTC ATTAAAGAAC AGAGCGTCAT
751 TAACCATTGT TACACCGAAA TTGATCTGAA GATTTTCCGT CAGTACCTCG
801 CTCCCGCGCT GGGTGTAAC TACCGCTTTG TCGGTACTGA ACCCTTTTGT
851 CGCGTTACCG CCCAGTACAA CCAGGATATG CGCTACTGGC TGGAAACGCC
901 GACTATCTCC GCACCGCCCA TCGAACTGGT TGAAATTGAG CGGCTGCGTT

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1101	AGACCCCCGC	ATGAGAAACA	GGTGAAAAAT	GAAAATAAAC	CAGCCCCGCC
1151	TTGCAGGCAC	CCTTGAGTCT	GGGGATGTGA	TGATACGCAT	CGCCCCACTC
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1951	CGGAAGGAAC	TGAACCTGCT	TTCGCACGCT	GTTCCATTTT	GCAGGCCGCG
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2751	GGCAGAACCG	GTGCAGATCC	ACTCTACGG	CGGTGCTGTG	CATCTGGTAC
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2901	CCTCGGCTAT	GCAATAGTTG	ATGCCGACAA	CGCAAAACAG	GTCGTGATGC
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3851	TTGTGCATCA	GGTGAAGGAA	TAAGCCATGC	ACCTGCTTCC	TGAACTCGCC
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4601	GGCTGGCTAC	CCCGTTTCAT	TGAATTTGGT	GCCTGTAGTG	CGGAAATGGC
4651	ACCAGAAAGCG	GTACTCCACG	GATTACGCC	AATTGGTATG	GCTTGCGAAG
4701	GTGATATGTT	CCGCGCCACT	GCGGGCGTAA	ACACGCATAA	AGGCAGCATT
4751	TTTTCTTTAG	GGCTGCTATG	TGCGGCAATT	GGCCGTTTGC	TTCAACTCAA
4801	CCAACCGGTA	ACGCCAACAA	CCGTTTGTTC	TACGGCGGCA	AGTTTCTGCC
4851	GTGGCCTGAC	CGATCGCGAA	CTGCGTACCA	ATAATTCAAC	ACTGACGGCA
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5151	AAGGGGGCAT	TCGAACCCCC	GCCGATCTCG	ATTATCTCCG	GCAGTTTCGAC
5201	AGGGAGTGTA	TCGAACGAAA	TCTCAGTCCA	GGCGGCAGTG	CTGACCTACT
		stop citG₁			
5251	GATCCTTACC	TGGTTTTTTAG	CACAGATTTA	ATTATTTAAG	CACTTGATAA
				r₁start citT	
5301	ATTTGGAAAT	ATTAATTTTC	GGAGAACCCG	TATGTCTTTA	GCAAAAGATA
5351	ATATATGGAA	ACTATTGGCC	CCACTGGTGG	TGATGGGTGT	CATGTTTCTT
5401	ATCCCTGTCC	CCGACGGTAT	GCCGCCGCAG	GCATGGCATT	ACTTCGCTGT
5451	GTTTGTGGCA	ATGATTGTCT	GCATGATCCT	CGAG	

INFORMATION FOR SEQ ID NO. 4:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 33 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

5'- AAATTTTCATATGCACCTGCTTCCTGAACTCGCC - 3'

INFORMATION FOR SEQ ID NO. 5:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 36 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

5'- GGGCCCCTCGAGTTAGTTGACGTTGCAGGCATCGAC - 3'

INFORMATION FOR SEQ ID NO. 6:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 553 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

1	ATGCACCTGC	TTCCTGAACT	CGCCAGCCAC	CATGCGGTAT	CAATTCCCGA
51	GCTGCTCGTC	AGCCGGGATG	AAAGGCAAGC	ACGGCAACAC	GTCTGGCTCA
101	AGCGCCATCC	TGTTCCACTG	GTCTCCTTTA	CCGTGGTTGC	GCCTGGGCCG
151	ATTAAAGACA	GCGAGGTCAC	ACGCCGAATT	TTTAATCATG	GCGTGACAGC
201	CTTGCGTGCC	TTAGCCGCAA	AACAGGGCTG	GCAAATTCAG	GAGCAGGCTG
251	CACTGGTTTC	CGCCAGCGGG	CCGGAGGGCA	TGTTGAGCAT	TGCCGCCCCG
301	GCTCGCGACC	TCAAGCTCGC	CACCATTGAG	CTTGAACATA	GTCATCCTCT
351	CGGGCGGTTA	TGGGATATCG	ATGTCCTGAC	GCCCCAAGGC	GAAATTCTCT
401	CCCGCCGCGA	CTATTCACTG	CCGCCTCGCC	GCTGCCTGTT	GTGCGAACAA
451	AGCGCAGCCG	TCTGCGCGCG	TGAAAAAACC	CATCAACTGA	CCGATTTACT
501	CAACCGCATG	GAGGCACTGC	TGAACGATGT	CGATGCCTGC	AACGTCAACT
551	AA				

INFORMATION FOR SEQ ID NO. 7:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 5593 base pairs
- (B) TYPE : nucleic acid
- (C) STRANDNESS : single
- (D) TOPOLOGY : linear

1 TTAATTAACA ACATAAAAAC CATAAAGCCA ATTAAGCCAC GAGAAAAACT GTGACTTAAA
61 TACAAGAATC CATAGCCGAA CGCTGGCGAA ATACAGTTCTG TTTTGAAATG ACGAAGCGCT

Start citCe

121 AAAAAATGAC ACTGATATTA AAACGCGTTC AGCTATTAAA AGATAAACCG CGGCGAGAGG
181 CGATCGATCG GTTTCTCCGC CAGCATCAAC TGTCGTTAGA GGCCGACTGC GAAATGGCGA
241 TTATCGCCGA GTATCAGCAG CGGCTGGTTC GCTGCGGTGC TATCGCCGGC AATGTGCTGA
301 AATGCATCGC CACGATCCC TCGTGCAGG GGGAGGGGCT GAGCCTTAAA TTAGTGACCG
361 AGCTCCTGAC GCTGGCCTAT GAGCTGGGGC GCAGCGAACT GTTTTTGTTC ACTAAACCTT
421 GCAATGCCGC GTTATTTTCC GGCGCCGGCT TCTGGCCGAT AGCCCAGGCG GGCGACCGCG
481 CCGTGCTAAT GGAAAATAGC CGCGAACGGC TGACTCGTTA CTGTGCACAG CTGGCGATGT
541 ACCGTCAGCC GGGAAGAAAA ATCGGCGCTA TCGTGATGAA TGCTAATCCA TTCACCCTCG
601 GCCACCGCTG GTTGGTAGAA CAGGCGGCCA GCCAGTGCAG CTGGCTGCAT CTGTTTGTGG
661 TCAAAGAAGA TGCGTCTGCT TTTTCCTATC ACGATCGCTT CAAGCTCATT GAACAGGGGA
721 TTACCGGCAT CGATAAGGTG ACGCTGCATC CCGGTTCCGC GTATCTGATC TCGCGGGCGA
781 CGTTCCCCGG CTATTTCTCT AAAGAGCAGG GGGTGGTTGA TGACTGCCAC AGCCAGATTG
841 ACCTGCAGCT CTTCCGCGAG CGCCTGGCCC CGGCGCTGCA GATTACCCAT CGCTTTGTCTG
901 GCACCGAGCC GCTGTGTCCC CTGACCCGTA ATTACAACCA GCGCATGAAG TCACTACTGG
961 AAGCGCCAGG CGACGCGCCG CCCATTGAAG TAGTTGAGCT TGCGCGAATC GAAAAAATG
1021 GTGGACCCGT GTCGGCCTCC CGAGTGCGCG AACTCTATCG ACAGCGCAAC TGGCAGGCGG
1081 TCGCGGCGCT GGTACCGCCG GGAACCCTCT CTTTTCTGAT GCAACTGGCG GAAAGCGAAC

Stop citCj

1141 ATCAAACCGC CTGATTTATA CGCCCTAACT AAGGATTTTC CCCTATGGAA ATGAAGATTG
1201 ACGCCCTGGC CGGCACGCTG GAGTCCAGCG ATGTGATGGT CAGGATTGGA CCCGCGGCGC
1261 AGCCGGGCAT TCAGCTGGAA ATCGACAGCA TTGTGAAACA ACAGTTTGGC GCTGCGATTG
1321 AGCAGGTAGT GAGAGAAACG CTGGCTCAGC TTGGCGTGAA ACAGGCCAAC GTGGTGGTCTG
1381 ATGATAAAGG CGCGCTGGAA TGTGTTTTGC GAGCTCGCGT ACAGGCCGCG GCGCTGCGCG

Stop citDj

1441 CGGCGCAACA GACCCAATTA CAATGGAGCC AGCTATGAAA CCACGTGCGA GTATGTTGTT

Start cite

1501 CATCCCTGGC GCCAATGCCG CCATGTAAAG CACGTCATTC GTCTACGGCG CTGATGCTGT
1561 GATGTTGAC CTGGAAGATG CCGTTTCGCT GCGCGAGAAA GATACCGCTC GTCTGCTGGT
1621 GTATCAGGCG CTGCAGCATC CACTGTATCA GGATATCGAA ACCGTGGTGC GTATTAACCC
1681 GCTAAATACC CCGTTTGGTC TGGCCGATCT GGAAGCCGTG GTTCGTGCGG GCGTGGATAT
1741 GGTGCGTCTG CCGAAAACCG ACAGCAAAGA AGATATCCAT GAGCTGGAAG CGCATGTTGA
1801 GCGGATTGAA CGCGAGTGCG GCCGGGAAGT GGGCAGCACC AAGTTAATGG CGGCGATCGA
1861 GTCGGCGCTG GCGGTGGTGA ACGCGGTGGA AATCGCCCGC GCCAGCCCGC GTCTGGCGGC
1921 GATCGCGCTG GCGGCCTTCG ATTACGTGAT GGATATGGGC ACCTCCCGCG GCGACGGTAC
1981 TGAATGTTT TACGCCCGCT GCGCTGTACT GCATGCCGCC CGCGTTGCCG GCATCGCCGC
2041 CTATGACGTG GTGTGGTCGG ATATCAATAA TGAAGAGGGC TTCCTGGCGG AAGCGAATCT
2101 GGCCAAAAAC CTCGGCTTTA ACGGCAAATC GTTGGTTAAC CCACGACAAA TTGAACTCCT
2161 GCATCAGGTC TATGCCCCGA CGCGCAAAGA GGTGATCAC GCGCTGGAAG TGATTGCCGC
2221 GCGCGAAGAA GCCGAAACGC GAGGTCTGGG TGTGGTATCG CTGAACGGCA AGATGATCGA
2281 TGGACCGATT ATCGACCATG CTCGCAAAGT GGTGGCGCTC TCGGCTTCCG GTATTCGTGA

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Stop	citE	Start	citF			
2341	TTAAGGGGAA	TAAGATGAAA	GAGACAGTAG	CAATGCTTAA	TCAGCAGTAC	GTGATGCCGA
2401	ATGGACTGAC	ACCTTATGCC	GGCGTAACGG	CGAAAAGTCC	CTGGCTGGCG	AGTGAGAGCG
2461	AAAAGCGCCA	GCGCAAAATC	TGCGATTTCG	TGGAAACGGC	AATCCGTCGC	TCCGGCCTGC
2521	AAAACGGCAT	GACCATCTCG	TTTCACCACG	CGTTTCGCGG	CGGTGACAAA	GTCGTCAATA
2581	TGGTAGTGGC	GAAGCTGGCG	GAAATGGGTT	TTCGCGATCT	CACCCTGGCG	TCCAGTTCGC
2641	TGATCGACGC	CCACTGGCCG	CTGATCGAGC	ATATTAAAA	TGGCGTGATC	CGCCAGATCT
2701	ACACCTCCGG	CCTGCGCGGC	AAGTTGGGCG	AGGAGATCTC	CGCCGGTTTA	ATGGAAAACC
2761	CGGTGCAGAT	CCACTCCAC	GGCGTTCGCG	TACAGCTGAT	TCAAAGCGGC	GAGCTGTGCA
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2881	GCGGTAAATC	ACGCTGCGGT	TCTCTGGGCT	ACGCGCGCGT	CGATGCCGAG	CACGCTAAAT
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3001	AGGATCAGGT	GGATCTGATA	GTCCAGGTAG	ATGAAGTCGG	CGATCCGCAA	AAAATTACCG
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3121	AAGTCGTTGA	GCACTCCGGT	TACTTTAAAG	AGGGTTTCTC	GCTGCAGACC	GGTACCGGCG
3181	GCGCCTCGCT	GGCAGTAACT	CGCTTCCTTG	AAGATAAAAT	GCGCCGTAAC	GGCATTACCG
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3301	TCAAAACGCT	GCTCGATACC	CAGTCCTTCG	ATGGTGACGC	GGCGCGTTCG	CTGGCGCAGA
3361	ACCCGAACCA	TGTCGAGATC	TCCACCAATC	AGTATGCCAG	CCCGGGCTCC	AAAGGCGCCT
3421	CCTGCGAGCG	CTTAAACGTG	GTGATGCTCA	GCGCGCTGGA	AATTGATATC	GACTTTAACG
3481	TTAACGTGAT	GACCGGTTCT	AACGGTGTGC	TGCGCGGGGC	GTCCGGTGCG	CATAGCGATA
3541	CCGCCGCCGG	TGCGGATTTG	ACCATTATTA	CCGCGCCGTT	AGTTCGCGGC	CGTATTCCCT
3601	GCGTCGTGGA	AAAGGTGCTG	ACCCGCGTCA	CGCCGGGGGC	CAGCGTGATG	TTGCTGGTCA
3661	CTGACCACGG	CATTGCGGTC	AACCCGGGAC	GATCGGACCT	GATCGACAAT	TTGCGCAGCG
3721	CAGGCATTCC	GCTGATGACC	ATTGAGGAAC	TGCAGCAGCG	TGCTGAGCTG	TTGACTGGCA
3781	AGCCGCAGCC	GATCGAATTC	ACCGATCGGG	TGGTGGCGGT	GGTGCGCTAT	CGCGACGGTT
				Stop		citF
3841	CGGTCATCGA	TGTGATTTCG	CAGGTGAAAA	ACAGCGACTA	AACGCAGAGG	GGAAAGGCCA
	citG					
3901	TGAGCGACGT	GTTAATTAAT	CCTGCGCGTG	TGCGGCGCGT	GAAGCCACTG	AGTGCCGAAG
3961	AGGTGGTCAG	CGCGGTAGAG	CGCGCGCTGT	TGACCGAAGT	TCGCCGTGAC	CCAAAGCCCG
4021	GGTTGGTGGA	TATTCGTAAC	GCTGGCGCGC	ACTGGGATAT	GGATCTGGCC	TCGTTTGAGG
4081	CCAGCACCGC	GGTGGTGGCT	CCGTGGATGG	AGAAATTTTT	CATCATGGGC	CACGATACTG
4141	CGGCGGTGCG	GCCGGAGCAG	GTATTGATGA	TGCTGCGCCC	GGTAGGGATG	GCCTGTGAGA
4201	ACGATATGCT	GGAGGCCACC	GGCGGGGTGA	ATACCCATCG	CGGGGCGATC	TTGCTTTTGG
4261	GCCTGCTCAG	CGCGGCGGCG	GGCAGGCTGG	TGTCGAAAGG	TGAGCCGATA	GAGCAGCACC
4321	GGCTTTGCGA	CCAGGTGGCG	CGCTTCTGTC	GCGGCATGGT	TATGCAGGAG	TTGTCTTCTG
4381	CTGGCGGGGA	ACGGCTCAGT	AAAGGCGAGG	CTCATTTTCT	ACGCTATGGT	CTCTCCGGGG
4441	CCCGCGGCGA	GGCGGAGAGC	GGTTTCCTGA	CGGTGCGTAC	CCAGGCCATG	CCAGTCTTTA
4501	CCCGCATGAT	GGAAGAGACC	GGCGACAGTA	ATCTGGCGCT	ACTGCAAACC	CTGCTGCATC
4561	TGATGGCGTG	GAATGATGAC	ACCAACCTGG	TCTCGCGCGG	CGGGCTTGCC	GGGCTGAACT
4621	TTGTCCAGCA	GGAGGCGCAG	CGACTGCTGT	GGCAGGGCGG	CGTGCTGGCG	GACGGCGGGC
4681	TGGAGGCGCT	GCGACAGTTT	GACGATGAGC	TGATTGCCCC	CCATCTCAGC	CCTGGCGGCA
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	Stop	citG				
4801	CGCTGTAACC	CACTGCAATA	CCGCCCTTCG	CCGCACTGTA	CGGGCGAGGG	CGCCATCATT
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4921	GATATCGTCC	GCCGTTTGTC	ATAAATTTCT	AATTATCGGC	GTTTTTGAGT	AGCGGCCCGC
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5041	ATGATGCACA	AATCCGCGTG	GCCATCGCCG	GCGCGGGCGG	CCGGATGGGA	CGCCAGTTAA
5101	TTCAGGCTGC	ATTGCAGATG	GAAGGCGTGG	CGCTGGGCGC	GGCGCTGGAG	CGCGAAGGGT
5161	CAAGCCTGGT	GGGCAGCGAC	GCCGGCGAGC	TGGCGGGCGC	CGGCAAAGCG	GGCGTCCGGG

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5221 TGCAGAGCAG CCTGGCGGGC GTAAAAGATG ATTTGACGCT GTTGATCGAT TTTACCCGCC
5281 CGGAAGGCAC GCTGAACCAT CTGGCGTTTT GCCGCGAGCA CGGCAAAGGG ATGGTCATCG
5341 GCACCACCGG TTTTGACGAC GCTGGCAAAC AGGCGATTCG CGATGCCGCG CAGGACATTG
5401 CCATTGTCTT CGCCGCTAAC TTTAGCGTTG GCGTCAATGT CCTGTTGAAG CTGCTGGAGA
5461 AGGCGGCGAA GGTGATGGGC GACTATACCG ACATCGAAAT TATCGAAGCG CACCACCGGC
5521 ATAAAGTGGA TGCGCCGTCA GGCACCGCGC TGGCGATGGG CGAAGCGATC GCCGGGGCAT
5581 TGAACAAAGA TCT

The invention is further elucidated by the following examples:

Example 1:

Cell culture

The following strains and plasmids were used: E. coli DH5 α or BL21 (DE3) (F.W. Studier and B.A. Mofatt, J. Mol. Biol. Vol. 189, 113-130 (1986)) and pACYC184 (A.C.Y. Chang et al., J. Bacteriol. Vol. 134, 1141-1156 (1978)). The E. coli cells were routinely cultured in Luria Bertani (LB) medium at 37°C according to J. Sambrook et al., Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (2nd Edition 1989). Antibiotics were added at the following final concentrations: 200 μ g/ml ampicillin, 50 μ g/ml chloroamphenicol and 50 μ g/ml kanamycin. The E. coli strain DH5 α was used as the host organism for the cloning. The E. coli BL21 (DE3) cells which contain the phage T7 polymerase gene under the control of a lacUV5 promoter (F.W. Studier and B.A. Moffatt, supra) served as a host for the expression of the target genes of pT7-7 and pET derivatives. The cultures for the expression were prepared as follows. After centrifugation (3000 g, 8 min) of a preculture of 40 ml which had been incubated overnight at 37°C, the cells were resuspended in 20 ml fresh LB medium. The cell suspension was subsequently

used to inoculate 2 L of the same medium which contained appropriate antibiotics and the culture was incubated at 37°C in a shaker (180 rpm). When the OD₆₀₀ reached a value between 0.5 and 0.8, the expression of the target genes was induced by adding IPTG (isopropyl-β-D-thiogalactoside) at a final concentration of 1 mM and the culture was incubated for a further 3 hours at 37°C in a shaker (180 rpm). Subsequently the cells were harvested by centrifugation (30 min at 3000 g), washed once with 20 ml 50 mM potassium phosphate, pH 7.0, 1 mM MgCl₂ and stored at -20°C.

Example 2:

Isolation of the genes and gene cluster

For the construction of the expression plasmid which contains the E. coli citCDEFXG gene cluster, a 6.9 kb fragment from the chromosomal DNA of E. coli was amplified by means of PCR with the primers eccl-for (SEQ ID NO.1) and ec-citT-rev (SEQ ID NO.2) using the Expand High Fidelity PCR System from Roche Diagnostics. The 6.9 kb PCR fragment which additionally contains the citT gene (K.M. Pos et al., J. Bacteriol. Vol. 180, 4160-4165 (1998)), was cleaved with the restriction endonucleases XbaI and XhoI and the resulting 5.5 kb fragment (SEQ ID NO.3) and an expression vector that was also linearized correspondingly such as pKK177-3Hb, pKKT5, pUC18, pT7, pET24b were separated on an agarose gel and the appropriate bands were isolated (QIAEX kit from the Diagen Company). Subsequently the PCR fragment and the vector fragment were ligated together using T4 DNA ligase. For this 1 µl (20 ng) vector fragment and 3 µl (100 ng) PCR fragment, 1 µl 10 x ligase buffer (Maniatis et al., 1989 B.27), 1 µl T4 DNA ligase, 4 µl sterile redistilled H₂O were pipetted, carefully mixed

and incubated overnight at 16°C. The insert obtained from the PCR starts 55 bp before the citC start codon and ends 203 bp downstream of the citG stop codon.

For the construction of the expression plasmid which contains the citX gene from E. coli (SEQ ID NO.3), the citX gene was amplified by PCR from the chromosomal DNA with the primers ec-citX-for (SEQ ID NO.4) and ec-citX-rev (SEQ ID NO.5) using the Pfu DNA polymerase (Stratagene). The start codon is part of an NdeI restriction endonuclease cleavage site and a XhoI restriction endonuclease cleavage site is located directly behind the stop codon. After digestion of the PCR product with NdeI and XhoI, the resulting 555 bp DNA fragment (SEQ ID NO.6) was ligated into appropriately linearized expression vectors (as described above).

The construction of the expression plasmid which contains the citCDEFG gene cluster of Klebsiella pneumoniae is described in M. Bott and P. Dimroth, Molecular Microbiology Vol. 14 (2), 347-356 (1994). The sequence of the citCDEFG gene cluster is shown in SEQ ID NO.7.

Example 3:

Transformation of the various expression plasmids in various E. coli expression strains

Competent cells of various E. coli strains were prepared according to the method of Hanahan (J. Mol. Biol. Vol. 166, 557 ff. (1983)). 200 µl of cells prepared in this manner were mixed with 20 ng of the corresponding expression plasmids. After 30 minutes incubation on ice, a heat shock was carried out (90 sec. at 42°C).

Subsequently the cells were transferred to 1 ml LB medium and incubated for 1 hour at 37°C for the phenotypic expression. Aliquots of this transformation mixture were plated on LB plates containing the appropriate antibiotic as a selection marker and incubated for 15 hours at 37°C.

Example 4:

Expression of the various target genes

After centrifugation (3000 g, 8 min) of 40 ml preculture which had been grown overnight at 37°C, the cell pellet was resuspended in 20 ml fresh LB medium. The cell suspension was then used to inoculate 2 l LB medium containing the appropriate antibiotics. This cell culture was incubated at 37°C in a shaker (180 rpm). The expression of the target genes was induced at an optical density (measured at 600 nm) of 0.5 - 0.8 by adding 1 mM isopropyl-β-D-thiogalactoside (IPTG, final concentration) and the cultures were incubated for a further 3 hours at 37°C and 180 rpm. Afterwards the cells were harvested by centrifugation (30 min. at 3000 g), washed once in 20 ml 50 mM potassium phosphate, pH 7.0 and frozen at -20°C.

For the cell extract preparation, 1 g cells (wet weight) were resuspended in 4 ml cold 50 mM potassium phosphate, 1 mM MgCl₂ pH 7.0. After adding a protease inhibitor cocktail (Roche Diagnostics) and DNaseI to a final concentration of 25 mg/ml, the cells were lysed by a three-fold passage in a French press at 108 Mpa. Intact cells and cell debris were removed by centrifugation (30 min. at 27,000 g). The cell-free supernatant was separated from the membrane fraction by ultracentrifugation (1 H at 150,000 g) and the resulting

cell extract can then be used directly for enzymatic studies and for protein purification.

Example 5:

Citrate lyase activity test

The citrate lyase activity was measured at 25°C in a spectrophotometric test coupled with malate dehydrogenase from Roche Diagnostics. The test mixture contained in a final volume of 1 ml 50 mM glycylglycine pH 7.9, 5 mM potassium citrate, 2 mM ZnCl_2 , 0.5 mM NADH, 30 U malate dehydrogenase (Roche Diagnostics) and 10 μl or 20 μl cell extract. The oxidation of NADH was measured in a spectrophotometer at 365 nm ($\epsilon = 3.4 \text{ mM}^{-1} \text{ cm}^{-1}$). One enzyme unit (unit) is defined as 1 μmol citrate which is degraded per minute to acetate and oxaloacetate.

SEQUENCE LISTING

<110> Roche Diagnostics GmbH

<120> Process for the recombinant production of holo-citrate lyase

<130> 523400EP

<140>

<141>

<160> 7

<170> PatentIn Ver. 2.1

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36

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38

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Claims

1. Process for the production of a protein with citrate lyase activity by expressing a suitable plasmid in a host organism and isolating the protein in an active form, wherein the plasmid contains the information from a gene cluster composed of at least six genes and an inducible promoter.
2. Process as claimed in claim 1, wherein the genes code for certain subunits of the protein having citrate lyase activity and/or for components that contribute to the biosynthesis of the complete enzyme.
3. Process as claimed in one of the claims 1 or 2, wherein the plasmid contains the genes citC, citD, citE, citF, citG and a DNA fragment obtainable from E. coli that is located between citF and citG on the E. coli citrate lyase gene cluster.
4. Process as claimed in claim 3, wherein the DNA fragment codes for a 20 kDa protein.
5. Process as claimed in claim 3 or 4, wherein the DNA fragment codes for a protein containing the motif G(A)-R-L-X-D-L(I)-D-V.

6. Process as claimed in one of the claims 1 to 5, wherein at least one gene is obtainable from *E. coli*, *Haemophilus influenzae*, *Klebsiella pneumoniae* or *Leuconostoc mesenteroides*.
7. Process as claimed in one of the claims 1 to 6, wherein at least four genes are derived from the microorganism that is specific for the isolated protein with citrate lyase activity.
8. Process as claimed in claim 7, wherein it is *Klebsiella pneumoniae*.
9. Process as claimed in one of the claims 1 to 8, wherein the host organism is a eukaryotic or prokaryotic microorganism.
10. Process as claimed in claim 9, wherein it is *E. coli*.
11. Process as claimed in one of the claims 1 to 10, wherein the expression occurs under aerobic conditions.
12. Recombinant soluble protein with citrate lyase activity and a molecular weight of about 14,000 to 15,000 Dalton obtainable by a process as claimed in one of the claims 1 to 11.
13. Test kit for the determination of citric acid which comprises essentially the following components

- (a) a protein with citrate lyase activity obtainable according to one of the claims 1 to 11,
 - (b) at least one protein with hydrogen-transferring activity
 - (c) nicotinamide adenine dinucleotide or a corresponding derivative in a reduced form and
 - (d) optionally suitable stabilizers, activators and/or substances to avoid or reduce interferences, and buffer solutions.
14. Test kit as claimed in claim 13, wherein L-malate dehydrogenase and optionally L-lactate dehydrogenase are used as the hydrogen-transferring enzymes.
15. Use of the enzyme obtainable according to claims 1 to 11 to determine citric acid.

Abstract

Process for the production of a protein with citrate lyase activity by expressing a suitable plasmid in a host organism and isolating the protein in an active form, wherein the plasmid contains the information from a gene cluster composed of at least six genes and an inducible promoter. Furthermore the invention concerns the use of the recombinant enzyme and a corresponding test kit for the determination of citric acid.

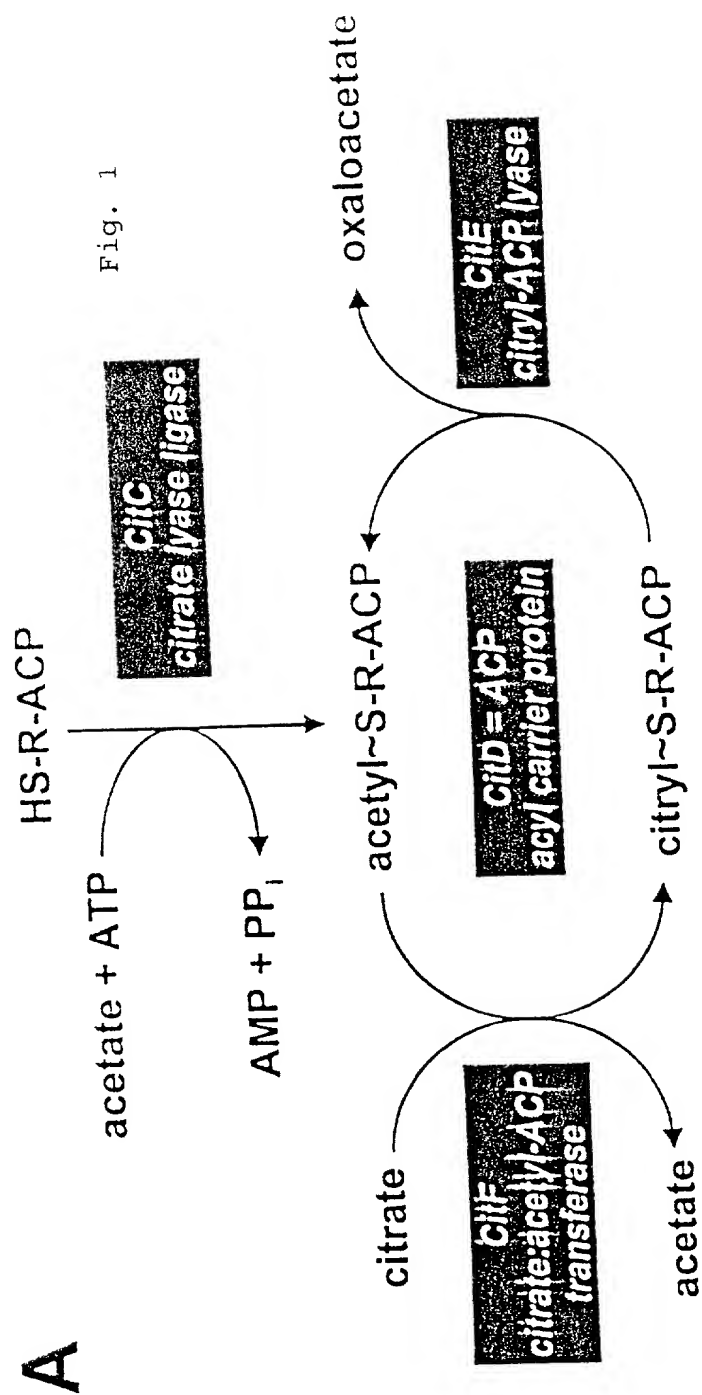


Fig. 1

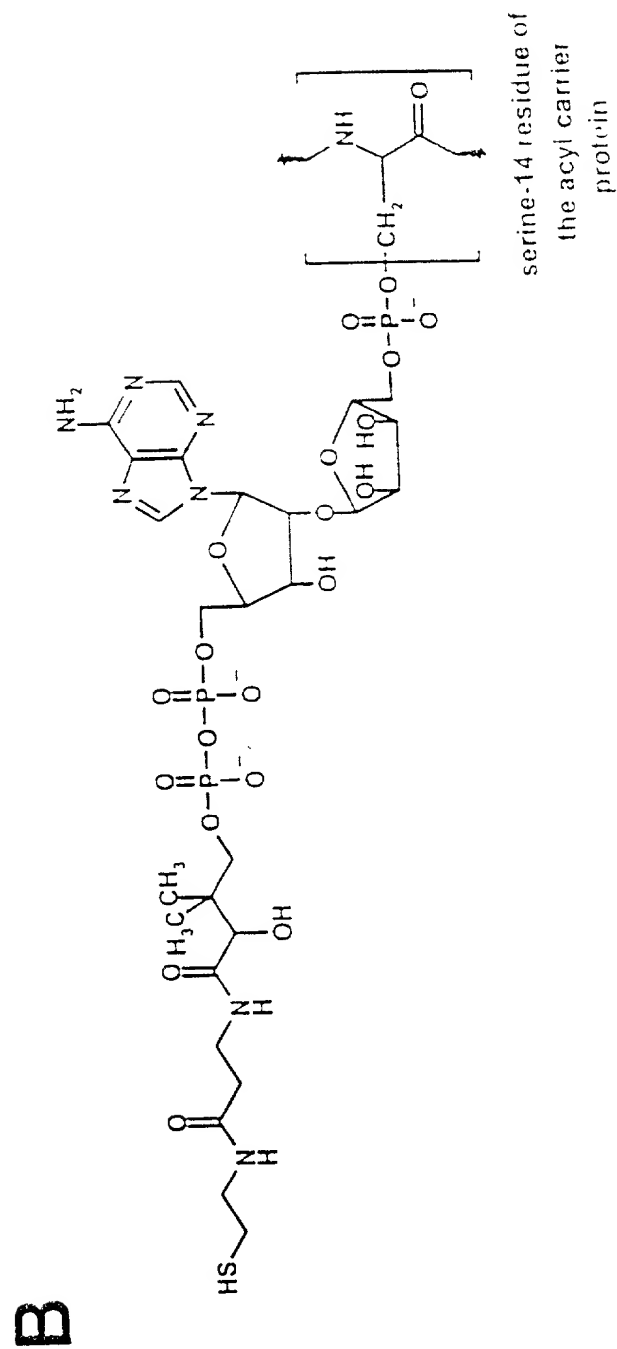
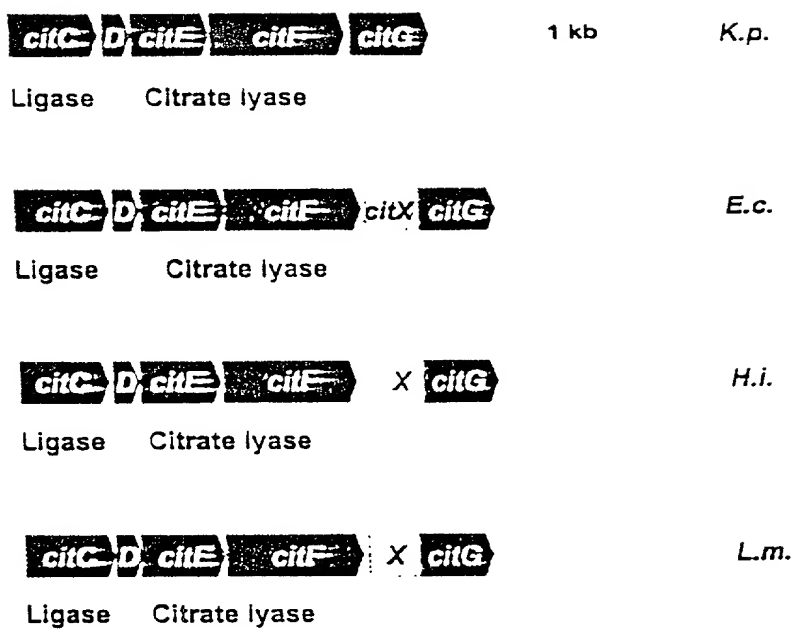


Fig. 2



Docket No.
BMID9975US

Declaration and Power of Attorney For Patent Application

English Language Declaration

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled
PROCESS FOR THE RECOMBINANT PRODUCTION OF HOLO-CITRATE LYASE

the specification of which

(check one)

☒ is attached hereto.

☐ was filed on _____ as United States Application No. or PCT International
Application Number _____
and was amended on _____
(if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)	Priority	Not Claimed
99119404.4 (Number)	Europe (Country)	30 September 1999 (Day/Month/Year Filed)
_____ (Number)	_____ (Country)	_____ (Day/Month/Year Filed)
_____ (Number)	_____ (Country)	_____ (Day/Month/Year Filed)

I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional application(s) listed below:

(Application Serial No.)

(Filing Date)

(Application Serial No.)

(Filing Date)

(Application Serial No.)

(Filing Date)

I hereby claim the benefit under 35 U. S. C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, C. F. R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. *(list name and registration number)*

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